CLAIMS

What is claimed is:

1. A method for identifying a test compound as a candidate for an antibiotic, comprising:
   a) contacting an OCTase polypeptide with a test compound; and
   b) detecting the presence or absence of binding between the test compound and the OCTase polypeptide, wherein binding indicates that the test compound is a candidate for an antibiotic.

2. The method of claim 1, wherein the OCTase polypeptide is a fungal OCTase polypeptide.

3. The method of claim 1, wherein the OCTase polypeptide is a *Magnaporthe* OCTase polypeptide.

4. The method of claim 1, wherein the OCTase polypeptide is SEQ ID NO:3.

5. A method for identifying a test compound as a candidate for an antibiotic, comprising:
   a) contacting a test compound with a polypeptide selected from the group consisting of:
      i) a polypeptide consisting essentially of SEQ ID NO:3;
      ii) a polypeptide having at least ten consecutive amino acids of SEQ ID NO:3;
      iii) a polypeptide having at least 50% sequence identity with SEQ ID NO:3 and at least 10% of the activity of SEQ ID NO:3; and
      iv) a polypeptide consisting of at least 50 amino acids having at least 50% sequence identity with SEQ ID NO:3 and at least 10% of the activity of SEQ ID NO:3; and
   b) detecting the presence and/or absence of binding between the test compound and the polypeptide, wherein binding indicates that the test compound is a candidate for an antibiotic.

6. A method for identifying a test compound as a candidate for an antibiotic, comprising:
   a) contacting carbamoyl phosphate and L-ornithine with an OCTase in the presence and absence of a test compound or contacting L-citrulline and phosphate with an OCTase in the presence and absence of a test compound; and
   b) determining a change in concentration for at least one of carbamoyl phosphate, L-ornithine, L-citrulline or phosphate in the presence and absence of the test compound, wherein a change in the concentration for any of carbamoyl phosphate, L-ornithine, L-citrulline and/or phosphate indicates that the test compound is a candidate for an antibiotic.

7. The method of claim 6, wherein the OCTase is a fungal OCTase.

8. The method of claim 7, wherein the OCTase is a *Magnaporthe* OCTase.

9. The method of claim 8, wherein the OCTase is SEQ ID NO:3.

10. A method for identifying a test compound as a candidate for an antibiotic, comprising:
   a) contacting an OCTase polypeptide with carbamoyl phosphate and L-ornithine in the presence and absence of a test compound or with L-citrulline and phosphate in the presence and absence of a test compound, wherein the OCTase polypeptide is selected from the group consisting of:
      i) a polypeptide having at least 50% sequence identity with SEQ ID NO:3 and at least 10% of the activity of SEQ ID NO:3,
      ii) a polypeptide consisting essentially of SEQ ID NO:3,
      iii) a polypeptide comprising at least 50 consecutive amino acids of SEQ ID NO:3 and having at least 10% of the activity of SEQ ID NO:3; and
      iv) a polypeptide consisting of at least 50 amino acids having at least 50% sequence identity with SEQ ID NO:3 and having at least 10% of the activity of SEQ ID NO:3; and

b) determining a change in concentration for at least one of carbamoyl phosphate, L-ornithine, L-citrulline and/or phosphate in the presence and absence of the test compound, wherein a change in the concentration for any of carbamoyl phosphate, L-ornithine, L-citrulline and/or phosphate indicates that the test compound is a candidate for an antibiotic.

11. A method for identifying a test compound as a candidate for an antibiotic, comprising:

a) measuring the expression of an OCTase in an organism, or a cell or tissue thereof, in the presence and absence of a test compound; and

b) comparing the expression of the OCTase in the presence and absence of the test compound, wherein an altered expression in the presence of the test compound indicates that the test compound is a candidate for an antibiotic.

12. The method of claim 11, wherein the organism is a fungus.

13. The method of claim 12, wherein the organism is *Magnaporthe.*

14. The method of claim 11, wherein the OCTase is SEQ ID NO:3.

15. The method of claim 11, wherein the expression of the OCTase is measured by detecting the OCTase mRNA.

16. The method of claim 11, wherein the expression of the OCTase is measured by detecting the OCTase polypeptide.

17. The method of claim 11, wherein the expression of the OCTase is measured by detecting the OCTase polypeptide enzyme activity.

18. A method for identifying a test compound as a candidate for an antibiotic, comprising:

a) providing a fungal organism having a first form of an OCTase;
b) providing a fungal organism having a second form of the OCTase, wherein one of the first or the second form of the OCTase has at least 10% of the activity of SEQ ID NO:3; and
c) determining the growth of the organism having the first form of the OCTase and the organism having the second form of the OCTase in the presence of a test compound,

wherein a difference in growth between the two organisms in the presence of the test compound indicates that the test compound is a candidate for an antibiotic.

19. The method of claim 18, wherein the fungal organism having the first form of the OCTase and the fungal organism having the second form of the OCTase are *Magnaporthe* and the first and the second form of the OCTase are fungal OCTases.

20. The method of claim 18, wherein the first form of the OCTase is SEQ ID NO:1 or SEQ ID NO:2.

21. The method of claim 18, wherein the fungal organism having the first form of the OCTase and the fungal organism having the second form of the OCTase are *Magnaporthe* and the first form of the OCTase is SEQ ID NO:1 or SEQ ID NO:2.

22. The method of claim 18, wherein the fungal organism having the first form of the OCTase and the fungal organism having the second form of the OCTase are *Magnaporthe*, the first form of the OCTase is SEQ ID NO:1 or SEQ ID NO:2, and the second form of the OCTase is a heterologous OCTase.

23. The method of claim 18, wherein the fungal organism having the first form of the OCTase and the fungal organism having the second form of the OCTase are *Magnaporthe*, the first form of the OCTase is SEQ ID NO:1 or SEQ ID NO:2, and the second form of the OCTase is SEQ ID NO:1 or SEQ ID NO:2 comprising a transposon insertion that reduces or abolishes OCTase activity.

24. A method for identifying a test compound as a candidate for an antibiotic, comprising:

a) providing a fungal organism having a first form of an OCTase;

b) providing a fungal organism having a second form of the OCTase, wherein one of the first or the second form of the OCTase has at least 10% of the activity of SEQ ID NO:3; and

c) determining the pathogenicity of the organism having the first form of the OCTase and the organism having the second form of the OCTase in the presence of a test compound,

wherein a difference in pathogenicity between the two organisms in the presence of the test compound indicates that the test compound is a candidate for an antibiotic.

25. The method of claim 24, wherein the fungal organism having the first form of the OCTase and the fungal organism having the second form of the OCTase are *Magnaporthe* and the first and the second form of the OCTase are fungal OCTases.

26. The method of claim 24, wherein the first form of the OCTase is SEQ ID NO:1 or SEQ ID NO:2.

27. The method of claim 24, wherein the fungal organism having the first form of the OCTase and the fungal organism having the second form of the OCTase are *Magnaporthe* and the first form of the OCTase is SEQ ID NO:1 or SEQ ID NO:2.

28. The method of claim 24, wherein the fungal organism having the first form of the OCTase and the fungal organism having the second form of the OCTase are *Magnaporthe*, the first form of the OCTase is SEQ ID NO:1 or SEQ ID NO:2, and the second form of the OCTase is a heterologous OCTase.

29. The method of claim 24, wherein the fungal organism having the first form of the OCTase and the fungal organism having the second form of the OCTase are

Magnaporthe, the first form of the OCTase is SEQ ID NO:1 or SEQ ID NO:2, and the second form of the OCTase is SEQ ID NO:1 or SEQ ID NO:2 comprising a transposon insertion that reduces or abolishes OCTase activity.

30. A method for identifying a test compound as a candidate for an antibiotic, comprising:
    a) providing a fungal organism having a first form of a gene in the arginine biosynthetic pathway;
    b) providing a fungal organism having a second form of said gene in the arginine biosynthetic pathway, wherein one of the first or the second form of the gene has at least 10% of the activity of a corresponding *Magnaportha grisea* gene; and
    c) determining the growth of the organism having the first form of the gene and the organism having the second form of the gene in the presence of a test compound,

wherein a difference in growth between the two organisms in the presence of the test compound indicates that the test compound is a candidate for an antibiotic.

31. The method of claim 30, wherein the fungal organism having the first form of the gene and the fungal organism having the second form of the gene are *Magnaporthe.*

32. The method of claim 30, wherein the fungal organism having the first form of the gene and the fungal organism having the second form of the gene are *Magnaporthe*, the first form of the gene in the arginine biosynthetic pathway is *Magnaporthe grisea* argininosucinate lyase, and the second form of the gene is a heterologous argininosucinate lyase.

33. The method of claim 30, wherein the fungal organism having the first form of the gene and the fungal organism having the second form of the gene are *Magnaporthe*, the first form of the gene in the arginine biosynthetic pathway is *Magnaporthe grisea* argininosucinate lyase, and the second form of the gene is *Magnaporthe grisea*

arginunosucinate lyase comprising a transposon insertion that reduces or abolishes arginunosucinate lyase protein activity.

34. The method of claim 30, wherein the fungal organism having the first form of the gene and the fungal organism having the second form of the gene are *Magnaporthe*, the first form of the gene in the arginine biosynthetic pathway is *Magnaporthe grisea* argininosuccinate synthase, and the second form of the gene is a heterologous argininosuccinate synthase.

35. The method of claim 30, wherein the fungal organism having the first form of the gene and the fungal organism having the second form of the gene are *Magnaporthe*, the first form of the gene in the arginine biosynthetic pathway is *Magnaporthe grisea* argininosuccinate synthase, and the second form of the gene is *Magnaporthe grisea* argininosuccinate synthase comprising a transposon insertion that reduces or abolishes argininosuccinate synthase protein activity.

36. A method for identifying a test compound as a candidate for an antibiotic, comprising:

a) providing a fungal organism having a first form of a gene in the arginine biosynthetic pathway;

b) providing a fungal organism having a second form of said gene in the arginine biosynthetic pathway, wherein one of the first or the second form of the gene has at least 10% of the activity of a corresponding *Magnaportha grisea* gene; and

c) determining the pathogenicity of the organism having the first form of the gene and the organism having the second form of the gene in the presence of a test compound,

wherein a difference in pathogenicity between the organism and the comparison organism in the presence of the test compound indicates that the test compound is a candidate for an antibiotic.

37. The method of claim 36, wherein the fungal organism having the first form of the gene and the fungal organism having the second form of the gene are *Magnaporthe*.

38. The method of claim 36, wherein the fungal organism having the first form of the gene and the fungal organism having the second form of the gene are *Magnaporthe*, the first form of the gene in the arginine biosynthetic pathway is *Magnaporthe grisea* argininosucinate lyase, and the second form of the gene is a heterologous argininosucinate lyase.

39. The method of claim 36, wherein the fungal organism having the first form of the gene and the fungal organism having the second form of the gene are *Magnaporthe*, the first form of the gene in the arginine biosynthetic pathway is *Magnaporthe grisea* argininosucinate lyase, and the second form of the gene is *Magnaporthe grisea* argininosucinate lyase comprising a transposon insertion that reduces or abolishes argininosucinate lyase protein activity.

40. The method of claim 36, wherein the fungal organism having the first form of the gene and the fungal organism having the second form of the gene are *Magnaporthe*, the first form of the gene in the arginine biosynthetic pathway is *Magnaporthe grisea* argininosuccinate synthase, and the second form of the gene is a heterologous argininosuccinate synthase.

41. The method of claim 36, wherein the fungal organism having the first form of the gene and the fungal organism having the second form of the gene are *Magnaporthe*, the first form of a gene in the arginine biosynthetic pathway is *Magnaporthe grisea* argininosuccinate synthase, and the second form of the gene is *Magnaporthe grisea* argininosuccinate synthase comprising a transposon insertion that reduces or abolishes acetylglutamate kinase/acetylglutamyl-phosphate reductase protein activity.

42. A method for identifying a test compound as a candidate for an antibiotic, comprising:

a) providing paired growth media containing a test compound, wherein the paired growth media comprise a first medium and a second medium and the second medium contains a higher level of L-arginine than the first medium;

b) innoculating the first and the second medium with an organism; and

c) determining the growth of the organism, wherein a difference in growth of the organism between the first and second medium indicates that the test compound is a candidate for an antibiotic.

43. The method of claim 42, wherein the organism is a fungus.

44. The method of claim 42, wherein the organism is *Magnaporthe.*